1. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
   (a) collecting a plasma sample from the HIV-infected patient;
   (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88; and
   (c) determining increased susceptibility to amprenavir.

2. The method of claim 1, wherein the mutation at codon 88 codes for a serine (S).

3. The method of claim 1, wherein the HIV-infected patient is being treated with an antiretroviral agent.

4. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
   (a) collecting a plasma sample from the HIV-infected patient;
   (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88 and additional mutations at codons 63 and/or 77 or a combination thereof; and
   (c) determining decreased susceptibilty to nelfinavir and indinavir and increased susceptibility to amprenavir.

5. The method of claim 4, wherein the mutation at codon 63 codes for a proline (P) or a glutamine (Q) and the mutation at codon 77 codes for an isoleucine (I).

6. The method of claim 4, wherein the HIV-infected patient is being treated with an antiretroviral agent.

7. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
   (a) collecting a plasma sample from the HIV-infected patient;
   (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88 and additional mutations at codons 63, 77 and/or 46 or a combination thereof; and
   (c) determining decreased susceptibilty to nelfinavir and indinavir and increased susceptibility to amprenavir.

8. The method of claim 7, wherein the mutation at codon 63 codes for a proline (P) or a glutamine (Q), the mutation at codon 77 codes for an isoleucine (I).and the mutation at codon 46 codes for a leucine (L) or an isoleucine (I).

9. The method of claim 7, wherein the HIV-infected patient is being treated with an antiretroviral agent.

10. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
   (a) collecting a plasma sample from the HIV-infected patient;
   (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88 and additional mutations at codons 63, 77, 46, 10, 20, and/or 36 or a combination thereof; and

(c) determining decreased susceptibilty to nelfinavir and indinavir and increased susceptibility to amprenavir.

11. The method of claim 10, wherein the mutation at codon 63 codes for a proline (P) or a glutamine (Q), the mutation at codon 77 codes for an isoleucine (I), the mutation at codon 46 codes for a leucine (L) or an isoleucine (I), the mutation at codon 10 codes for a isoleucine (I) or a phenylalanine (F), the mutation at 20 codes for a threonine (T) or a methionine (M) or an arginine (R), and the mutation at 36 codes for an isoleucine (I) or a valine (V).

12. The method of claim 10, wherein the HIV-infected patient is being treated with an antiretroviral agent.

13. A method for evaluating the biological effectiveness of a candidate HIV antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 88 and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

14. A method for evaluating the biological effectiveness of a candidate HIV antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 88 and mutation(s) at codons 63 and/or 77 or a combination thereof and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug copound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

15. A method for evaluating the biological effectiveness of a candidate HIV antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 88 and mutation(s) at codons 63, 77, and/or 46 or a combination thereof and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

16. A method for evaluating the biological effectiveness of a candidate HIV antiretroviral drug compound comprising:
    (a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 88 and mutation(s) at codons 63, 77, 46, 10, 20, and/or 36 or a combination thereof and an indicator gene into a host cell;
    (b) culturing the host cell from step (a);
    (c) measuring the indicator in a target host cell; and
    (d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

17. A resistance test vector comprising an HIV — patient-derived segment further comprising protease having a mutation at codon 88 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient derived segment.

18. The resistance test vector of claim 17, wherein the patient-derived segment having a mutation at codon 88 further comprises mutations at codons 63 and 77 or a combination thereof.

19. The resistance test vector of claim 17, wherein the patient-derived segment having a mutation at codon 88 further comprises mutations at codons 63, 77 and/or 46

or a combination thereof.

20. The resistance test vector of claim 17, wherein the patient-derived segment having a mutation at codon 88 further comprises mutations at codons 63, 77, 46, 10, 20 and/or 36 or a combination thereof.

21. A method for evaluating the viral fitness of a patient's virus comprising:

(a) introducing a resistance test vector comprising a patient-derived segment from a patient's virus and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the luciferase activity in a target host cell in the absence of any antiretroviral drug; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a)-(c) are carried out for a reference control in the absence of any antiretroviral drug;

wherein a reduction in the luciferase activity measured in step (c) as compared to step (d) indicates a reduction in viral fitness.

22. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and secondary positions; and

(c) determining changes in susceptibility to ritonavir, nelfinavir, indinavir, saquinivir and amprenavir.

23. The method of claim 22, wherein the mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

24. The method of claim 22, wherein the HIV-infected patient is being treated with an antiretroviral agent.

25. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
    (a) collecting a plasma sample from the HIV-infected patient;
    (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 24; and
    (c) determining decreased susceptibilty to indinavir.

26. The method of claim 25, wherein the mutation at codon 24 codes for an isoleucine (I).

27. The method of claim 25, wherein the HIV-infected patient is being treated with an antiretroviral agent.

28. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
    (a) collecting a plasma sample from the HIV-infected patient;
    (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 71; and
    (c) determining decreased susceptibilty to indinavir.

29. The method of claim 28, wherein the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine, (T) valine, (V) leucine (L) and isoleucine (I).

30. The method of claim 28, wherein the HIV-infected patient is being treated with an antiretroviral agent.

31. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
(a) collecting a plasma sample from the HIV-infected patient;
(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and additional mutations at codons selected from the group consisting of codon 54, 46, 10, 63, and a combination thereof; and
(c) determining decreased susceptibilty to indinavir.

32. The method of claim 31, wherein the mutation at codon 54 codes for an amino acid selected from the group consisting of a valine (V), alanine (A), leucine (L) and threonine (T), the mutation at codon 46 codes for an amino acid selected from the group consisting of a leucine (L), isoleucine (I) and valine (V), the mutation at codon 10 codes for an amino acid selected from the group consisting of an isoleucine (I), valine (V), phenylalanine (F), and arginine (R), and the mutation at codon 63 codes for an amino acid selected from the group consisting of proline (P), alanine (A), serine (S), threonine (T), glutamine(Q), , cysteine (C),and valine (V).

33. The method of claim 31, wherein the HIV-infected patient is being treated with an antiretroviral agent.

34. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 20; and

() determining decreased susceptibilty to saquinavir.

35. The method of claim 34, wherein the mutation at codon 20 codes for an amino acid selected from the group consisting of a methionine (M), threonine (T), isoleucine (I), and arginine (R).

36. The method of claim 34, wherein the HIV-infected patient is being treated with an antiretroviral agent.

37. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 36; and

() determining decreased susceptibilty to saquinavir.

38. The method of claim 37, wherein the mutation at codon 36 for an amino acid selected from the group consisting of a isoleucine (I), leucine (L), and valine (V).

39. The method of claim 37, wherein the HIV-infected patient is being treated with an antiretroviral agent.

40. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and additional mutations at codons 24, 71, 54, and/or 10 or a combination thereof; and

(c) determining decreased susceptibilty to saquinavir.

41. The method of claim 40, wherein the mutation at codon 24 codes for an isoleucine (I), the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine (T), valine (V), leucine (L), and isoleucine (I), the mutation at codon 54 codes for an amino acid selected from the group consisting of valine (V), alanine (A), leucine (L), and threonine (T), and the mutation at codon 10 codes for an amino acid selected from the group consisting of an isoleucine (I), valine (V), phenylalanine (F), and arginine(R).

42. The method of claim 40, wherein the HIV-infected patient is being treated with an antiretroviral agent.

43. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
   (a) collecting a plasma sample from the HIV-infected patient;
   (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and the number of additional mutations at secondary positions; and
   (c) determining decreased susceptibilty to indinavir and saquinavir.

44. The method of claim 43, wherein the number of additional mutations at secondary positions is at least 3.

45. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
   (a) collecting a plasma sample from the HIV-infected patient;
   (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and secondary mutations; and
   (c) determining changes in susceptibility to ritonavir, nelfinavir, indinavir, saquinivir and amprenavir.

46. The method of claim 45, wherein the mutation at codon 90 codes for a methionine.

47. The method of claim 45, wherein the HIV-infected patient is being treated with an antiretroviral agent.

48. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
    (a) collecting a plasma sample from the HIV-infected patient;
    (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 73; and
    (c) determining decreased susceptibilty to indinavir.

49. The method of claim 48, wherein the mutation at codon 73 codes for an amino acid selected from the group consisting of a serine (S), threonine (T), and cysteine (C).

50. The method of claim 48, wherein the HIV-infected patient is being treated with an antiretroviral agent.

51. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
    (a) collecting a plasma sample from the HIV-infected patient;
    (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 71; and
    (c) determining decreased susceptibilty to indinavir.

52. The method of claim 51, wherein the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine (T), valine (V), leucine (L), and isoleucine (I).

53. The method of claim 51, wherein the HIV-infected patient is being treated with an antiretroviral agent.

54. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
    (a) collecting a plasma sample from the HIV-infected patient;
    (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 46,; and
    (c) determining decreased susceptibilty to indinavir.

55. The method of claim 54, wherein the mutation at codon 46 codes for an amino acid selected from the group consisting of a leucine (L), isoleucine (I) and valine (V).

56. The method of claim 54, wherein the HIV-infected patient is being treated with an antiretroviral agent.

57. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
    (a) collecting a plasma sample from the HIV-infected patient;
    (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 73; and
    (c) determining decreased susceptibilty to saquinavir.

58. The method of claim 57, wherein the mutation at codon 73 codes for an amino acid selected from the group consisting of a serine (S), threonine (T), and cysteine (C).

59. The method of claim 57, wherein the HIV-infected patient is being treated with an antiretroviral agent.

60. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
(a) collecting a plasma sample from the HIV-infected patient;
(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 71; and
(c) determining decreased susceptibilty to saquinavir.

61. The method of claim 60, wherein the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine (T), valine (V), leucine (L), and isoleucine (I).

62. The method of claim 60, wherein the HIV-infected patient is being treated with an antiretroviral agent.

63. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
(a) collecting a plasma sample from the HIV-infected patient;
(b) evaluating whether the plasma sample contains

nucleic acid encoding HIV protease having a mutation at codon 90 and additional mutations at codons 77 and 10; and

() determining decreased susceptibilty to saquinavir.

64. The method of claim 63, wherein the mutation at codon 77 codes for an amino acid selected from the group consisting of isoleucine (I) and threonine (T) and the mutation at codon 10 codes for an amino acid selected from the group consisting of isoleucine (I), valine (V), phenylalanine (F), and arginine (R).

65. The method of claim 63, wherein the HIV-infected patient is being treated with an antiretroviral agent.

66. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and the number of additional mutations at secondary positions; and

(c) determining decreased susceptibilty to indinavir and saquinavir.

67. The method of claim 66, wherein the number of additional mutations at secondary positions is at least 3.

68. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected

patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codons 82 and 90 and secondary mutations; and

(c) determining changes in susceptibility to ritonavir, nelfinavir, indinavir, saquinivir and amprenavir.

69. The method of claim 68, wherein the mutation at codon 82 codes for an amino acid selected from the group consisting of alanine (A), phenylalanine (F), serine (S), and threonine (T) and the mutation at codon 90 codes for a methionine (M).

70. The method of claim 68, wherein the HIV-infected patient is being treated with an antiretroviral agent.

71. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 82 and additional mutations at one or more secondary positions and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

72. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 82 and secondary mutation(s) at codons 20, 24, 71, 54 and/or 10 or a combination thereof and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

73. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 90 and additional mutations at one or more secondary positions and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator

measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

74. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 90 and secondary mutation(s) at codons 73, 71, 10 and/or 46 or a combination thereof and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

75. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codons 82 and 90 and additional mutations at one or more secondary positions and

an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

76. A resistance test vector comprising an HIV patient-derived segment further comprising protease having a mutation at codon 82 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient derived segment.

77. The resistance test vector of claim 76, wherein the patient-derived segment having a mutation at codon 82 further comprises at least one secondary mutation at a codon selected from the group consisting of 20, 24, 71, 54, 10 and a combination thereof.

78. The resistance test vector of claim 76, wherein the patient-derived segment having a mutation at codon 90 further comprises at least one secondary mutation at a codon selected from the group consisting of 73, 71, 46, 10 and a combination thereof.

79. A method for determining replication capacity for a patient's virus comprising:

(a) introducing a resistance test vector comprising a patient derived segment and an indicator gene into

a host cell;

(b) culturing the host cell from (a);

(c) harvesting viral particles from step (b) and infecting target host cells;

(d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment;

(e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector; and

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

80. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient;

(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 or codon 90; and

(c) determining changes in susceptibility to protease inhibitors.

81. The method of claim 80, wherein step (c) determines changes in susceptibility to saquinavir.

82. The method of claim 80, wherein the mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

83. The method of claim 82, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F),

serine (S), or threonine (T) for valine(V).

84. The method of claim 80, wherein the mutation at codon 90 codes for methionine (M).

85. The method of claim 84, wherein the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

86. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

(a) introducing a resistance test vector comprising a patient-derived segment having nucleic acid encoding HIV protease with a mutation at codon 82 or codon 90 and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator gene in a target host cell; and

(d) comparing the measurement of the indicator gene from step (c) with the measurement of the indicator gene measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

87. A resistance test vector comprising an HIV patient-derived segment further comprising protease having a mutation at codon 82 or codon 90 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

88. The resistance test vector of claim 87, wherein the patient-derived segment having a mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

89. The resistance test vector of claim 88, wherein the patient-derived segment having a mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V).

90. The resistance test vector of claim 87, wherein the patient-derived segment having a mutation at codon 90 codes for methionine (M).

91. The resistance test vector of claim 90, wherein the patient-derived segment having a mutation at codon 90 is a substitution of methionine (M) for leucine (L).

92. A method for determining replication capacity for a patient's virus comprising:

(a) introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell;

(b) culturing the host cell from (a);

(c) harvesting viral particles from step (b) and infecting target host cells;

(d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment; and

(e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector.

93. The method of claim 92 further comprising the step of:

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

94. The method of claim 92 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 66.

95. The method of claim 92 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 154.

96. The method of claim 94 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 153.

97. The method of claim 94 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 154.

98. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient;

(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71,

64, 93, 23, 58, and 36; and

(c) determining a change in susceptibility to a protease inhibitor.

99. The method of claim 98, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

100. The method of claim 99, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

101. The method of claim 100, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, 90, 32 and 39 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 20, 71, 64 and 93, wherein the protease inhibitor is saquinavir.

102. The method of claim 101, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 20, and 71, wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

103. The method of claim 101, having a mutation at codon 82 and a secondary mutation at codons 32 or 39, or a mutation at codon 90 and a secondary mutation at codons 64 or 93, wherein the change in susceptibility in step

(c) is an increase in susceptibility to saquinavir.

104. The method of claim 100, having a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, and 74, wherein the protease inhibitor is indinavir.

105. The method of claim 104, having a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, and 46, wherein the change in susceptibility in step (c) is a decrease in susceptibility to indinavir.

106. The method of claim 104, having a mutation at codon 90 and a secondary mutation at codons 13 or 74, wherein the change in susceptibility in step (c) is an increase in susceptibility to indinavir.

107. The method of claim 100, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 48, 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.

108. The method of claim 107, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

109. The method of claim 108, wherein step (c) is determining a change in susceptibility to the protease inhibitor greater than 10 fold.

110. The method of claim 108, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 48, 23, 84, 53, 74, 20, 60, 33, 36, 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 84, 53, 48, 23, 58, 20, 36, and 54, wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

111. The method of claim 108, having a mutation at codon 82 and a secondary mutation at codons 32 or 46, or a mutation at codon 90 and a secondary mutation at codons 64, 77, or 93, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

112. The method of claim 108, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, and 62, wherein the change in susceptibility in step (c) is a decrease in susceptibility to indinavir.

113. The method of claim 108, having a mutation at codon 82 and a secondary mutation at codon 13, or a mutation at codon 90 and a secondary mutation at codon 74, wherein the change in susceptibility in step (c) is an increase in susceptibility to indinavir.

114. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient;

(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and secondary mutations of at least three codons; and

(c) determining a decrease in susceptibility to saqinavir.

115. The method of claim 114, wherein in the evaluating step (b), the nucleic acid encoding HIV protease has secondary mutations of at least five codons.

116. The method of claim 114, wherein the secondary mutation are selected from the group consisting of codons 10, 20, 52, 53, 54, 66, 71, 73 and 84.

117. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient;

(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 61, 11, and 46, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69; and

(c) determining a change in susceptibility to amprenavir.

118. The method of claim 117, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F),

serine (S), or threonine (T) for valine(V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

119. The method of claim 118, having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 11, and 46, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 47, 66, 32, 55, 53, and 13; wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

120. The method of claim 118, having a mutation at codon 82 and a secondary mutation at codon 61, or a mutation at codon 90 and secondary mutations at codons 74, 15, or 69, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

121. A resistance test vector comprising an HIV patient-derived segment comprising nucleic acid encoding protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

122. The resistance test vector of claim 121, wherein the mutation of the patient derived segment at codon 82 is

a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

TABLE A

Summary of Replication Capacity (RC) and Enzyme Function Results

	LOW RC (<25% of Ref.*)	MEDIUM RC (26-75% of Ref.)	HIGH RC (>75% of Ref.)
% of Total Tested	41% (55)	45% (59)	14% (19)
PR Processing Defects (%p41>10%)	71% (39)	24% (14)	10% (2)
Impaired RT Activity (<25% of reference)	14% (7)	2% (1)	0%
>10 mutations in Protease	62% (34)	22% (13)	5% (1)
>10X reduced susceptibility to NFV	63% (35)	32% (19)	16% (3)

*Reference virus: NL4-3